

1642

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/493,480

DATE: 03/07/2001
 TIME: 12:56:47

ENTERED

Input Set : A:\-98-1.app
 Output Set: N:\CRF3\03072001\I493480.raw

3 <110> APPLICANT: Cheever, Martin A.
 4 Gheysen, Dirk
 5 Corixa Corporation
 6 SmithKline Beecham Biologicals S. A.
 8 <120> TITLE OF INVENTION: HER-2/neu Fusion Proteins
 10 <130> FILE REFERENCE: 014058-009810PC
 12 <140> CURRENT APPLICATION NUMBER: US 09/493,480
 13 <141> CURRENT FILING DATE: 2000-01-28
 15 <150> PRIOR APPLICATION NUMBER: US 60/117,976
 16 <151> PRIOR FILING DATE: 1999-01-29
 18 <160> NUMBER OF SEQ ID NOS: 26
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1255
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Homo sapiens
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 28 <223> OTHER INFORMATION: human HER-2/neu protein
 30 <220> FEATURE:
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 32 <222> LOCATION: (1)..(653)
 33 <223> OTHER INFORMATION: extracellular domain (ECD)
 35 <220> FEATURE:
 36 <221> NAME/KEY: DOMAIN
 37 <222> LOCATION: (676)..(1255)
 38 <223> OTHER INFORMATION: intracellular domain (ICD)
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 41 <221> NAME/KEY: DOMAIN
 42 <222> LOCATION: (990)..(1255)
 43 <223> OTHER INFORMATION: phosphorylation domain (PD)
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 46 <221> NAME/KEY: DOMAIN
 47 <222> LOCATION: (990)..(1048)
 48 <223> OTHER INFORMATION: fragment of the phosphorylation domain, preferred
 49 portion (delta PD)
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 53 1 5 10 15
 55 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
 56 20 25 30
 58 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
 59 35 40 45
 61 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
 62 50 55 60
 64 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
 65 65 70 75 80
 67 Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu

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68          85          90          95
70 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
71          100          105          110
73 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
74          115          120          125
76 Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
77          130          135          140
79 Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
80 145          150          155          160
82 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
83          165          170          175
85 Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
86          180          185          190
88 His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
89          195          200          205
91 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
92          210          215          220
94 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
95 225          230          235          240
97 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
98          245          250          255
100 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
101          260          265          270
103 Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
104          275          280          285
106 Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
107          290          295          300
109 Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
110 305          310          315          320
112 Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
113          325          330          335
115 Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
116          340          345          350
118 Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
119          355          360          365
121 Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
122          370          375          380
124 Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
125 385          390          395          400
127 Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
128          405          410          415
130 Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
131          420          425          430
133 Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
134          435          440          445
136 Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
137          450          455          460
139 Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
140 465          470          475          480

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142 Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
143           485           490           495
145 Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
146           500           505           510
148 Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
149           515           520           525
151 Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
152           530           535           540
154 Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
155 545           550           555           560
157 Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
158           565           570           575
160 Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
161           580           585           590
163 Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
164           595           600           605
166 Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
167           610           615           620
169 Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
170 625           630           635           640
172 Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser
173           645           650           655
175 Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly
176           660           665           670
178 Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg
179           675           680           685
181 Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
182           690           695           700
184 Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
185 705           710           715           720
187 Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
188           725           730           735
190 Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile
191           740           745           750
193 Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu
194           755           760           765
196 Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg
197           770           775           780
199 Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu
200 785           790           795           800
202 Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg
203           805           810           815
205 Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly
206           820           825           830
208 Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
209           835           840           845
211 Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe
212           850           855           860
214 Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp

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215 865      870      875      880
217 Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
218      885      890      895
220 Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
221      900      905      910
223 Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
224      915      920      925
226 Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
227      930      935      940
229 Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
230 945      950      955      960
232 Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe
233      965      970      975
235 Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
236      980      985      990
238 Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
239      995      1000      1005
241 Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu
242      1010      1015      1020
244 Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly
245 1025      1030      1035      1040
247 Gly Met Val His His Arg His Arg Ser Ser Thr Arg Ser Gly Gly
248      1045      1050      1055
250 Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro Arg
251      1060      1065      1070
253 Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly
254      1075      1080      1085
256 Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His
257      1090      1095      1100
259 Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu
260 1105      1110      1115      1120
262 Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln
263      1125      1130      1135
265 Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro
266      1140      1145      1150
268 Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
269      1155      1160      1165
271 Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val
272      1170      1175      1180
274 Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
275 1185      1190      1195      1200
277 Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala
278      1205      1210      1215
280 Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala
281      1220      1225      1230
283 Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
284      1235      1240      1245
286 Leu Gly Leu Asp Val Pro Val
287      1250      1255

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300 <222> LOCATION: (1)..(654)
301 <223> OTHER INFORMATION: extracellular domain (ECD)
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316 <223> OTHER INFORMATION: phosphorylation domain (PD)
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319 <221> NAME/KEY: DOMAIN
320 <222> LOCATION: (991)..(1049)
321 <223> OTHER INFORMATION: fragment of the phosphorylation domain, preferred
322     portion (delta PD)
324 <400> SEQUENCE: 2
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328 Pro Pro Gly Ile Ala Gly Thr Gln Val Cys Thr Gly Thr Asp Met Lys
329           20               25               30
331 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
332           35               40               45
334 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
335           50               55               60
337 Val Pro Ala Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
338   65               70               75               80
340 Gln Gly Tyr Met Leu Ile Ala His Asn Gln Val Lys Arg Val Pro Leu
341           85               90               95
343 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Lys Tyr
344           100              105              110
346 Ala Leu Ala Val Leu Asp Asn Arg Asp Pro Gln Asp Asn Val Ala Ala
347           115              120              125
349 Ser Thr Pro Gly Arg Thr Pro Glu Gly Leu Arg Glu Leu Gln Leu Arg
350           130              135              140
352 Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Arg Gly Asn Pro
353   145              150              155              160
355 Gln Leu Cys Tyr Gln Asp Met Val Leu Trp Lys Asp Val Phe Arg Lys

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VERIFICATION SUMMARY
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